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Appendix 2: CLUSTAL W (1.83) multiple sequence alignment

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O43759_SYNGR1a      MEGGAYGAGKAG-GAFDPYTLVRQPHTILRVVSWLFSIVVFGSIVNEGYLNSASEGEEFC
O43759_SYNGR1b      MEGGAYGAGKAG-GAFDPYTLVRQPHTILRVVSWLFSIVVFGSIVNEGYLNSASEGEEFC
O43759_SYNGR1c      MLTLEFGILEFDPSWIGSWTOR9WVSWRSRPGCELFSIVVFGSIVNEGYLNSASEGEEFC
SEQ_ID_297           MEGGAYGAGKAG-GAFDPYTLVRQPHTILRVVSWLFSIVVFGSIVNEGYLNSASEGEEFC
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O43759_SYNGR1a      IYNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSDIGVSAFWAFLW
O43759_SYNGR1b      IYNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSDIGVSAFWAFLW
O43759_SYNGR1c      IYNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSDIGVSAFWAFLW
SEQ_ID_297           IYNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSDIGVSAFWAFLW
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O43759_SYNGR1a      FVGFCYLANQWQVSKPKDNPLNEGTDAAARAIAFSFFSIFTWAGQAVLAFQRYQIGADSA
O43759_SYNGR1b      FVGFCYLANQWQVSKPKDNPLNEGTDAAARAIAFSFFSIFTWSLTAALAVRREKDLSEQE
O43759_SYNGR1c      FVGFCYLANQWQVSKPKDNPLNEGTDAAARAIAFSFFSIFTWSLTAALAVRREKDLSEQE
SEQ_ID_297           FVGFCYLANQWQVSKPKDNPLNEGTDAAARAIAFSFFSIFTWSLTAALAVRREKDLSEQE
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O43759_SYNGR1a      LFSQDYMDPSQDSSMPYAPYVEPNTGPDPAAGMGTYQQPANTFDTEPQGYQSQGY
O43759_SYNGR1b      EYSTLFPASAQP-----
O43759_SYNGR1c      EYSTLFPASAQP-----
SEQ_ID_297           EYSTLFPASAQP-----
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